

=====

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=4; day=13; hr=17; min=2; sec=7; ms=359;]

=====

Application No: 10566409

Version No: 2.0

Input Set:

Output Set:

Started: 2009-03-20 18:24:37.386

Finished: 2009-03-20 18:24:55.179

Elapsed: 0 hr(s) 0 min(s) 17 sec(s) 793 ms

Total Warnings: 631

Total Errors: 9

No. of SeqIDs Defined: 699

Actual SeqID Count: 699

| Error code | Error Description |
|------------|---|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (19) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (20) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (27) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (28) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (29) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (30) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (31) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (32) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (33) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (34) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (35) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (36) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (37) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (38) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (39) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (40) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (41) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (42) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (43) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (44) |

Input Set:

Output Set:

Started: 2009-03-20 18:24:37.386
Finished: 2009-03-20 18:24:55.179
Elapsed: 0 hr(s) 0 min(s) 17 sec(s) 793 ms
Total Warnings: 631
Total Errors: 9
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

| Error code | Error Description |
|------------|---|
| | This error has occurred more than 20 times, will not be displayed |
| W 402 | Undefined organism found in <213> in SEQ ID (201) |
| W 402 | Undefined organism found in <213> in SEQ ID (202) |
| W 402 | Undefined organism found in <213> in SEQ ID (203) |
| W 402 | Undefined organism found in <213> in SEQ ID (204) |
| W 402 | Undefined organism found in <213> in SEQ ID (205) |
| W 402 | Undefined organism found in <213> in SEQ ID (206) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (212) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (216) |
| W 402 | Undefined organism found in <213> in SEQ ID (451) |
| W 402 | Undefined organism found in <213> in SEQ ID (452) |
| W 402 | Undefined organism found in <213> in SEQ ID (457) |
| W 402 | Undefined organism found in <213> in SEQ ID (458) |
| W 251 | Found intentionally skipped sequence in SEQID (520) |
| W 251 | Found intentionally skipped sequence in SEQID (521) |
| W 251 | Found intentionally skipped sequence in SEQID (522) |
| W 251 | Found intentionally skipped sequence in SEQID (523) |
| W 251 | Found intentionally skipped sequence in SEQID (524) |
| W 251 | Found intentionally skipped sequence in SEQID (525) |
| W 251 | Found intentionally skipped sequence in SEQID (526) |
| W 251 | Found intentionally skipped sequence in SEQID (527) |
| W 251 | Found intentionally skipped sequence in SEQID (639) |

Input Set:

Output Set:

Started: 2009-03-20 18:24:37.386
Finished: 2009-03-20 18:24:55.179
Elapsed: 0 hr(s) 0 min(s) 17 sec(s) 793 ms
Total Warnings: 631
Total Errors: 9
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

| Error code | Error Description |
|------------|--|
| W 251 | Found intentionally skipped sequence in SEQID (640) |
| W 251 | Found intentionally skipped sequence in SEQID (643) |
| W 251 | Found intentionally skipped sequence in SEQID (646) |
| W 251 | Found intentionally skipped sequence in SEQID (680) |
| W 251 | Found intentionally skipped sequence in SEQID (681) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (685) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (685) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (685) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (696) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (696) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (696) |
| E 257 | Invalid sequence data feature in <221> in SEQ ID (696) |
| W 251 | Found intentionally skipped sequence in SEQID (699) |

<110> Ledbetter, Jeffrey A.
Hayden-Ledbetter, Martha S.
Thompson, Peter A.

<120> BINDING CONSTRUCTS AND METHODS FOR USE THEREOF

<130> 910180.40102USPC

<140> 10566409

<141> 2009-03-20

<150> PCT/US2003/041600

<151> 2003-12-24

<150> US 10/627,556

<151> 2003-07-26

<150> US 10/053,530

<151> 2002-01-17

<150> US 60/367,358

<151> 2001-01-17

<160> 699

<170> PatentIn version 3.2

<210> 1

<211> 714

<212> DNA

<213> Homo sapiens

<400> 1

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| tctgatcagg | agcccaaata | ttgtgacaaa | actcacacat | gcccaccgtg | cccagcacct | 60 |
| gaactcctgg | ggggaccgtc | agtcttcttc | ttccccccaa | aaccaagga | caccctcatg | 120 |
| atctcccgga | cccctgaggt | cacatgcgtg | gtggtggacg | tgagccacga | agaccctgag | 180 |
| gtcaagtcca | actggtacgt | ggacggcggtg | gaggtgcata | atgccaaagac | aaagccgcgg | 240 |
| gaggagcagt | acaacagcac | gtaccgtgtg | gtcagcgtcc | tcaccgtcct | gcaccaggac | 300 |
| tggtgaatg | gcaaggagta | caagtgcaag | gtctccaaca | aagccctccc | agccccatc | 360 |
| gagaaaacaa | tctccaaagc | caaagggcag | ccccgagaac | cacaggtgta | caccctgccc | 420 |
| ccatccccggg | atgagctgac | caagaaccag | gtcagcctga | cctgcctggt | caaaggcttc | 480 |
| tatcccagcg | acatcgccgt | ggagtgggag | agcaatgggc | agccggagaa | caactacaag | 540 |
| accacgcctc | ccgtgctgga | ctccgacggc | tccttcttcc | tctacagcaa | gtcaccgtg | 600 |
| gacaagagca | ggtggcagca | ggggaacgtc | ttctcatgct | ccgtgatgca | tgaggetctg | 660 |
| cacaaccact | acacgcagaa | gagcctctcc | ctgtctccgg | gtaaatagatc | taga | 714 |

<210> 2

<211> 235

<212> PRT

<213> Homo sapiens

<400> 2

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asp | Gln | Glu | Pro | Lys | Ser | Cys | Asp | Lys | Thr | His | Thr | Cys | Pro | Pro |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser | Val | Phe | Leu | Phe | Pro |
| | | | | 20 | | | | 25 | | | | | 30 | | |
| Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr | Pro | Glu | Val | Thr |
| | | | | 35 | | | 40 | | | | | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu | Val | Lys | Phe | Asn |
| 50 | | | | | | 55 | | | | | 60 | | | | |
| Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala | Lys | Thr | Lys | Pro | Arg |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val | Ser | Val | Leu | Thr | Val |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys | Cys | Lys | Val | Ser |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr | Ile | Ser | Lys | Ala | Lys |
| | | 115 | | | | | 120 | | | | | | 125 | | |
| Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu | Pro | Pro | Ser | Arg | Asp |
| | | 130 | | | | | 135 | | | | | | 140 | | |
| Glu | Leu | Thr | Lys | Asn | Gln | Val | Ser | Leu | Thr | Cys | Leu | Val | Lys | Gly | Phe |
| 145 | | | | 150 | | | | | | 155 | | | | | 160 |
| Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp | Glu | Ser | Asn | Gly | Gln | Pro | Glu |
| | | | | 165 | | | | | | 170 | | | | | 175 |
| Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val | Leu | Asp | Ser | Asp | Gly | Ser | Phe |
| | | | 180 | | | | | | 185 | | | | | 190 | |
| Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp | Lys | Ser | Arg | Trp | Gln | Gln | Gly |
| | | | 195 | | | | | 200 | | | | | | 205 | |
| Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala | Leu | His | Asn | His | Tyr |
| | | 210 | | | | | 215 | | | | | 220 | | | |
| Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly | Lys | | | | | |
| 225 | | | | | | 230 | | | | | | | | | 235 |

<210> 3

<211> 718

<212> DNA

<213> Lama glama

<220>

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<220>

<221> modified_base

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<223> n is a, c, g, or t

<220>

<221> modified_base

<222> (52)..(52)

<223> n is a, c, g, or t

<220>

<221> modified_base

<222> (55)..(55)

<223> n is a, c, g, or t

<220>

<221> modified_base

<222> (58)..(58)

<223> n is a, c, g, or t

<220>

<221> modified_base

<222> (64)..(64)

<223> n is a, c, g, or t

<400> 3

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|------------|------------|------------|------------|------------|------------|-----|
| tgatcaagaa | ccacatggag | gatgcacgtg | ccncagtg | ccncaatgcc | cngcncnga | 60 |
| actnccagga | ggcccttctg | tctttgtctt | ccccccgaaa | cccaaggacg | tcctctccat | 120 |
| ttttggaggc | cgagtcacgt | gcgttgtagt | ggacgtcggg | aagaaagacc | ccgaggtcaa | 180 |

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|-----|
| tttcaactgg | tatattgatg | gcgttgaggt | gcgaacggcc | aatacgaagc | caaaagagga | 240 |
| acagtccaac | agcacgtacc | gcgtggtcag | cgctctgccc | atccagcacc | aggactggct | 300 |
| gacggggaag | gaattcaagt | gcaaggtcaa | caacaaagct | ctcccggccc | ccatcgagag | 360 |
| gaccatctcc | aaggccaag | ggcagacccg | ggagccgcag | gtgtacaccc | tggccccaca | 420 |
| ccgggaagaa | ctggccaagg | acaccgtgag | cgtaacatgc | ctgggtcaaag | gcttctaccc | 480 |
| agctgacatc | aacgttgagt | ggcagaggaa | cggtcagccg | gagtcagagg | gcacctacgc | 540 |
| caacacgccg | ccacagctgg | acaacgacgg | gacctacttc | ctctacagca | agctctcggt | 600 |
| gggaaagaac | acgtggcagc | ggggagaaac | cttaacctgt | gtggtgatgc | atgaggccct | 660 |
| gcacaaccac | tacaccacaga | aatccatcac | ccagtcttcg | ggtaaatagt | aatctaga | 718 |

<210> 4

<211> 231

<212> PRT

<213> Lama glama

<400> 4

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | His | Gly | Gly | Cys | Thr | Cys | Pro | Gln | Cys | Pro | Ala | Pro | Glu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Pro | Gly | Gly | Pro | Ser | Val | Phe | Val | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Ser | Ile | Ser | Gly | Arg | Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Lys | Glu | Asp | Pro | Glu | Val | Asn | Phe | Asn | Trp | Tyr | Ile | Asp | Gly | Val |
| 50 | | | | | | 55 | | | | | 60 | | | | |
| Glu | Val | Arg | Thr | Ala | Asn | Thr | Lys | Pro | Lys | Glu | Gln | Phe | Asn | Ser | |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Thr | Tyr | Arg | Val | Val | Ser | Val | Leu | Pro | Ile | Gln | His | Gln | Asp | Trp | Leu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Gly | Lys | Glu | Phe | Lys | Cys | Lys | Val | Asn | Asn | Lys | Ala | Leu | Pro | Ala |
| | | | 100 | | | | | | 105 | | | | 110 | | |
| Pro | Ile | Glu | Arg | Thr | Ile | Ser | Lys | Ala | Lys | Gly | Gln | Thr | Arg | Glu | Pro |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Gln | Val | Tyr | Thr | Leu | Ala | Pro | His | Arg | Glu | Glu | Leu | Ala | Lys | Asp | Thr |
| 130 | | | | | | 135 | | | | | 140 | | | | |
| Val | Ser | Val | Thr | Cys | Leu | Val | Lys | Gly | Phe | Tyr | Pro | Ala | Asp | Ile | Asn |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Val | Glu | Trp | Gln | Arg | Asn | Gly | Gln | Pro | Glu | Ser | Glu | Gly | Thr | Tyr | Ala |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Asn | Thr | Pro | Pro | Gln | Leu | Asp | Asn | Asp | Gly | Thr | Tyr | Phe | Leu | Tyr | Ser |
| | | | 180 | | | | | | 185 | | | | 190 | | |
| Arg | Leu | Ser | Val | Gly | Lys | Asn | Thr | Trp | Gln | Arg | Gly | Glu | Thr | Leu | Thr |
| | 195 | | | | | 200 | | | | | 205 | | | | |
| Gly | Val | Val | Met | His | Glu | Ala | Leu | His | Asn | His | Tyr | Thr | Gln | Lys | Ser |
| 210 | | | | | 215 | | | | | | 220 | | | | |
| Ile | Thr | Gln | Ser | Ser | Gly | Lys | | | | | | | | | |
| 225 | | | | | 230 | | | | | | | | | | |

<210> 5

<211> 757

<212> DNA

<213> Lama glama

<400> 5

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| tgatcaagaa | cccaagacac | caaaaccaca | accacaacca | caaccacaac | ccaatcctac | 60 |
| aacagaatcc | aagtgtccca | aatgtccagc | ccctgagctc | ctgggagggc | cctcagtctt | 120 |
| catcttcccc | ccgaaccca | aggacgtcct | ctccatttct | gggaggcccg | aggtcacgtg | 180 |
| cgttgtggta | gacgtgggcc | aggaagaccc | cgaggtcagt | ttcaactggg | acattgatgg | 240 |
| cgctgaggtg | cgaacggcca | acacgaggcc | aaaagaggaa | cagttcaaca | gcacgtaccg | 300 |
| cgtggtcagc | gtcctgcccc | tccagcacca | ggactggctg | acggggaagg | aattcaagtg | 360 |

| | | | | | | |
|------------|------------|-------------|-------------|------------|------------|-----|
| caaggtcaac | aacaaagctc | tcccggcccc | catcgagaag | accatctcca | aggccaaagg | 420 |
| gcagaccggg | gagccgcagg | tgtacaccct | ggccccacac | cggaagagc | tggccaagga | 480 |
| caccgtgagc | gtaacatgcc | tgggtcaaagg | cttctaccca | cctgatatca | acgttgagtg | 540 |
| gcagaggaat | gggcagccgg | agtcagaggg | cacytacgcc | accacgccac | cccagctgga | 600 |
| caacgacggg | acctacttcc | tctacagcaa | gctctcgggtg | ggaaagaaca | cgtggcagca | 660 |
| gggagaaacc | ttcacctgtg | tgggtgatgca | cgaggccctg | cacaaccact | acacccagaa | 720 |
| atccatcacc | cagtcttcgg | gtaaatagta | atctaga | | | 757 |

<210> 6

<211> 248

<212> PRT

<213> Lama glama

<400> 6

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gln | Glu | Pro | Lys | Thr | Pro | Lys | Pro | Gln | Pro | Gln | Pro | Gln | Pro | Gln |
| 1 | | | | 5 | | | | 10 | | | | 15 | | | |
| Pro | Asn | Pro | Thr | Thr | Glu | Ser | Lys | Cys | Pro | Lys | Cys | Pro | Ala | Pro | Glu |
| | | | 20 | | | | | 25 | | | | 30 | | | |
| Leu | Leu | Gly | Gly | Pro | Ser | Val | Phe | Ile | Phe | Pro | Pro | Lys | Pro | Lys | Asp |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Leu | Ser | Ile | Ser | Gly | Arg | Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Gly | Gln | Glu | Asp | Pro | Glu | Val | Ser | Phe | Asn | Trp | Tyr | Ile | Asp | Gly |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Ala | Glu | Val | Arg | Thr | Ala | Asn | Thr | Arg | Pro | Lys | Glu | Glu | Gln | Phe | Asn |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| Ser | Thr | Tyr | Arg | Val | Val | Ser | Val | Leu | Pro | Ile | Gln | His | Gln | Asp | Trp |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Leu | Thr | Gly | Lys | Glu | Phe | Lys | Cys | Lys | Val | Asn | Asn | Lys | Ala | Leu | Pro |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Pro | Ile | Glu | Lys | Thr | Ile | Ser | Lys | Ala | Lys | Gly | Gln | Thr | Arg | Glu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Pro | Gln | Val | Tyr | Thr | Leu | Ala | Pro | His | Arg | Glu | Glu | Leu | Ala | Lys | Asp |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Thr | Val | Ser | Val | Thr | Cys | Leu | Val | Lys | Gly | Phe | Tyr | Pro | Pro | Asp | Ile |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Asn | Val | Glu | Trp | Gln | Arg | Asn | Gly | Gln | Pro | Glu | Ser | Glu | Gly | Thr | Tyr |
| | | 180 | | | | | 185 | | | | | | 190 | | |
| Ala | Thr | Thr | Pro | Pro | Gln | Leu | Asp | Asn | Asp | Gly | Thr | Tyr | Phe | Leu | Tyr |
| | | 195 | | | | 200 | | | | | | 205 | | | |
| Ser | Lys | Leu | Ser | Val | Gly | Lys | Asn | Thr | Trp | Gln | Gln | Gly | Glu | Thr | Phe |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Thr | Cys | Val | Val | Met | His | Glu | Ala | Leu | His | Asn | His | Tyr | Thr | Gln | Lys |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| Ser | Ile | Thr | Gln | Ser | Ser | Gly | Lys | | | | | | | | |
| | | | | | 245 | | | | | | | | | | |

<210> 7

<211> 727

<212> DNA

<213> Lama glama

<400> 7

| | | | | | | |
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| actccttgga | gggcccacgg | tcttcattctt | ccccccgaaa | gccaaggacg | tcctctccat | 120 |
| caccggaaaa | cctgaggtca | cgtgcttggtg | gtggacgtgg | gtaaagaaga | ccctgagatc | 180 |
| gagttcaagc | tgggtccgtgg | atgacacaga | ggtagacacg | gctgagacaa | agccaaagga | 240 |
| ggaacagttc | aacagcacgt | accgcgtgggt | cagcgtcctg | cccatccagc | accaggactg | 300 |
| gctgacgggg | aaggaattca | agtgcaaggt | caacaacaaa | gctctcccag | cccccatcga | 360 |


```

gaggaccatc tccaaggcca aagggcagac cggggagccg caggtgtaca ccctggcccc 420
acaccgggaa gagctggcca aggacaccgt gagcgtaacc tgcctgggtca aaggcttctt 480
cccagctgac atcaacgttg agtggcagag gaatgggcag ccggagtcag agggcaccta 540
cgccaacacg ccgccacagc tggacaacga cgggacctac ttcctctaca gcaaactctc 600
cgtgggaaag aacacgtggc agcagggaga agtcttcacc tgtgtggtga tgcacgagggc 660
tctacacaat cactccaccc agaaatccat caccagtcct tcgggtaaat agtaatctag 720
agggcccc 727

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<210> 8

<211> 236

<212> PRT

<213> Lama glama

<400> 8

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Asp Gln Ala His His Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys
1          5          10          15
Pro Gly Pro Glu Leu Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro
          20          25          30
Lys Ala Lys Asp Val Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys
          35          40          45
Leu Trp Trp Thr Trp Val Lys Lys Thr Leu Arg Ser Ser Ser Ser Trp
          50          55          60
Ser Val Asp Asp Thr Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu
65          70          75          80
Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln
          85          90          95
His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
          100          105          110
Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly
          115          120          125
Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu
          130          135          140
Leu Ala Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe
145          150          155          160
Pro Ala Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser
          165          170          175
Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr
          180          185          190
Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln
          195          200          205
Gly Glu Val Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His
          210          215          220
Ser Thr Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
225          230          235

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<210> 9

<211> 54

<212> DNA

<213> Homo sapiens

<400> 9

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<210> 10

<211> 18

<212> PRT

<213> Homo sapiens

<400> 10

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Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys

```

```

1              5              10              15
Pro Ala

<210> 11
<211> 54
<212> DNA
<213> Homo sapiens
<400> 11
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<210> 12
<211> 18
<212> PRT
<213> Homo sapiens
<400> 12
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      1              5              10              15
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<210> 13
<211> 327
<212> DNA
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<400> 13
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      gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg          180
      cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag          240
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<210> 14
<211> 109
<212> PRT
<213> Homo sapiens
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      20              25              30
      Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
      35              40              45
      Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
      50              55              60
      Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
      65              70              75              80
      Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
      85              90              95
      Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
      100              105

<210> 15
<211> 324
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gacggctcct tcttctctta tagcaagctc accgtggaca agagcaggtg gcagcagggg 240
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Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
          20          25          30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
          35          40          45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
          50          55          60
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65          70          75          80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
          85          90          95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 17
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<210> 18
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 <212> PRT
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1          5          10          15
Pro Ala

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ccggaccctt gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa 180
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